```
   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
     AGTGCATTTT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
   1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                              ^STII Signal Sequence TIR-1                                Anti-Tissue Factor Light Chain^

 501 CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACTGGT
     GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA
  26 Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  R  D  I  K  S  Y  L  N  W  Y

 601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
     TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
  60   Q  Q  K  P  G  K  A  P  K  V  L  I  Y  Y  A  T  S  L  A  E  G  V  P  S  R  F  S  G  S  G  S  G  T

 701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
     CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCCT CTCAGAGGTA CCTGTAAACC TGTCCCATGG
 .93  D  Y  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  L  Q  H  G  E  S  P  W  T  F  G  Q  G  T

 801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
     TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
 126 K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L

 901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
 160   N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K

1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P  V  T  K  S  F  N  R  G  E  C  O
```

FIG. 1A

```
1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
     GCGTTATACC GCGTTTTACT GGTTGTCGCC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCG GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
     TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT
     ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTTT CCCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
                                                                                  M  K  K  N  I  A  F  L  L
   1                                                                              ^STII Signal Sequence TIR-1

1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
     ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
  10 A  S  M  F  V  F  S  I  A  T  N  A  Y  A  E  V  Q  L  V  E  S  G  G  G  L  V  Q  P  G  G  S  L  R
                                                ^Anti-Tissue Factor Heavy Chain

1701 TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA TTGATTGATC
     AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT AACTAACTAG
  43 L  S  C  A  A  S  G  F  N  I  K  E  Y  Y  M  H  W  V  R  Q  A  P  G  K  G  L  E  W  V  G  L  I  D  P

1801 CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
     GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGCGAC TGTTAAGGTT TTTGTGTCGT ATGGACGTCT ACTTGTCGGA
  77  E  Q  G  N  T  I  Y  D  P  K  F  Q  D  R  A  T  I  S  A  D  N  S  K  N  T  A  Y  L  Q  M  N  S  L

1901 GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCTGG TCACCGTCTC CTCGGCCTCC
     CGCACGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCCAGTT CCTTGGGACC AGTGGCAGAG GAGCCGGAGG
 110  R  A  E  D  T  A  V  Y  Y  C  A  R  D  T  A  A  Y  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S  A  S

2001 ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC
     TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA GTTCCTGATG AAGGGGCTTG
 143  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C  L  V  K  D  Y  F  P  E  P

2101 CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
     GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA
 177  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCCAAATCT
     CTGACACGGG AGATCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT TCTTTCAACT CGGGTTTAGA
 210  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K  V  E  P  K  S

2301 TGTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA ACCCAAGGAC ACCCTCATGA
     ACACTGTTTT GAGTGTGTAC GGGTGGCACG GGTCGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGGTTT TGGGTTCCTG TGGGAGTACT
 243  C  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T  L  M  I

2401 TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA
     AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC CTGCCGCACC TCCACGTATT
 277  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N
```

FIG. 1B

```
2501 TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
     ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCCTGA CCGACTTACC GTTCCTCATG
 310 A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y

2601 AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC
     TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CGGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG TGTCCACATG TGGGACGGGG
 343 K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P

2701 CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA
     GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGGTCGCT GTAGCGGCAC CTCACCCTCT CGTTACCCGT
 377  S  R  E  E  M  T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q

2801 GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
     CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC TGTTCTCGTC CACCGTCGTC
 410  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q

2901 GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATAAGCA TGCGACGGCC
     CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCCC ATTTATTCGT ACGCTGCCGG
 443 G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  O

3001 CTAGAGTCCC TAACGCTCGG TTGCCGCCGG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG
     GATCTCAGGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAAACTGT CGAATAGTAG CTATTCGAAA TTACGCCATC AAATAGTGTC

3101 TTAAATTGCT AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG TCACCCTGGA TGCTGTAGGC ATAGGCTTGG
     AATTTAACGA TTGCGTCAGT CCGTGGCACA TACTTTAGAT TGTTACGCGA GTAGCAGTAG GAGCCGTGGC AGTGGGACCT ACGACATCCG TATCCGAACC
                                      ^Start Tet Resistance Coding Sequence

3201 TTATGCCGGT ACTGCCGGGC CTCTTGCGGG ATATCGTCCA TTCCGACAGC ATCGCCAGTC ACTATGGCGT GCTGCTAGCG CTATATGCGT TGATGCAATT
     AATACGGCCA TGACGGCCCG GAGAACGCCC TATAGCAGGT AAGGCTGTCG TAGCGGTCAG TGATACCGCA CGACGATCGC GATATACGCA ACTACGTTAA

3301
```

FIG. 1C

```
   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAAAACATC GCTTTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
     AGTGCATTTT TCCCATAGAT CTTAATACTT CTTTTTGTAG CGAAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
   1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                              ^start STII signal TIR~2                                          start light chain^

 501 CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACTGGT
     GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA
  26 Q  M  T  Q   S  P  S   S  L  S   A  S  V  G   D  R  V   T  I  T   C  R  A  S   R  D  I   K  S  Y   L  N  W  Y

 601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
     TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
  60   Q  Q  K   P  G  K   A  P  K  V   L  I  Y   Y  A  T   S  L  A  E   G  V  P   S  R  F   S  G  S  G   S  G  T

 701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
     CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCCT CTCAGAGGTA CCTGTAAACC TGTCCCATGG
  93  D  Y  T   L  T  I  S   S  L  Q   P  E  D   F  A  T  Y   Y  C  L   Q  H  G   E  S  P  W   T  F  G   Q  G  T

 801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
     TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
 126 K  V  E  I   K  R  T   V  A  A   P  S  V  F   I  F  P   P  S  D   E  Q  L  K   S  G  T   A  S  V   V  C  L  L

 901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
 160   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N   A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K

1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T   Y  S  L  S   S  T  L   T  L  S   K  A  D   Y  E  K  H   K  V  Y   A  C  E  V   T  H  Q   G  L  S
```

FIG. 2A

```
1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T   Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y   A  C  E  V   T  H  Q   G  L  S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P  V  T   K  S  F   N  R  G   E  C  O

1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
     GCGTTATACC GCGTTTTACT GGTTGTCGCC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCG GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
     TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAAAACATCG CTTTTCTTCT
     ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTTT CCCATAGATC TTAATACTTC TTTTTGTAGC GAAAAGAAGA
   1                                                                                    M  K   K  N  I  A   F  L  L
                                                                                       ^start STII signal TIR-2

1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
     ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
  10  A  S  M   F  V  F  S   I  A  T   N  A  Y   A  E  V  Q   L  V  E   S  G  G   G  L  V  Q   P  G  G   S  L  R
                                                 ^start heavy chain

1701 TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA TTGATTGATC
     AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT AACTAACTAG
  43 L  S  C  A   A  S  G   F  N  I   K  E  Y  Y   M  H  W   V  R  Q   A  P  G  K   G  L  E   W  V  G   L  I  D  P

1801 CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
     GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGCGAC TGTTAAGGTT TTTGTGTCGT ATGGACGTCT ACTTGTCGGA
  77   E  Q  G   N  T  I   Y  D  P  K   F  Q  D   R  A  T   I  S  A  D   N  S  K   N  T  A   Y  L  Q  M   N  S  L

1901 GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCTGG TCACCGTCTC CTCGGCCTCC
     CGCACGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCCAGTT CCTTGGGACC AGTGGCAGAG GAGCCGGAGG
 110  R  A  E   D  T  A  V   Y  Y  C   A  R  D   T  A  A  Y   F  D  Y   W  G  Q   G  T  L  V   T  V  S   S  A  S

2001 ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT CAAGGACTAC TTCCCCGAAC
     TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA GTTCCTGATG AAGGGGCTTG
 143 T  K  G  P   S  V  F   P  L  A   P  S  S  K   S  T  S   G  G  T   A  A  L  G   C  L  V   K  D  Y   F  P  E  P

2101 CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
     GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA
 177   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S   S  G  L   Y  S  L  S   S  V  V
```

FIG. 2B

```
2101 CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
     GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACCA
 177   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S   S  G  L   Y  S  L  S   S  V  V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCCAAATCT
     CTGACACGGG AGATCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT TCTTTCAACT CGGGTTTAGA
 210   T  V  P   S  S  S  L   G  T  Q   T  Y  I   C  N  V  N   H  K  P   S  N  T   K  V  D  K   K  V  E   P  K  S

2301 TGTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA ACCCAAGGAC ACCCTCATGA
     ACACTGTTTT GAGTGTGTAC GGGTGGCACG GGTCGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGGTTT TGGGTTCCTG TGGGAGTACT
 243 C  D  K  T   H  T  C   P  P  C   P  A  P  E   L  L  G   G  P  S   V  F  L  F   P  P  K   P  K  D   T  L  M  I

2401 TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA
     AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC CTGCCGCACC TCCACGTATT
 277   S  R  T   P  E  V   T  C  V  V   V  D  V   S  H  E   D  P  E  V   K  F  N   W  Y  V   D  G  V  E   V  H  N

2501 TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
     ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCCTGA CCGACTTACC GTTCCTCATG
 310   A  K  T   K  P  R  E   E  Q  Y   N  S  T   Y  R  V  V   S  V  L   T  V  L   H  Q  D  W   L  N  G   K  E  Y

2601 AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC
     TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CGGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG TGTCCACATG TGGGACGGGG
 343 K  C  K  V   S  N  K   A  L  P   A  P  I  E   K  T  I   S  K  A   K  G  Q  P   R  E  P   Q  V  Y   T  L  P  P

2701 CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA
     GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGGTCGCT GTAGCGGCAC CTCACCCTCT CGTTACCCGT
 377   S  R  E   E  M  T   K  N  Q  V   S  L  T   C  L  V   K  G  F  Y   P  S  D   I  A  V   E  W  E  S   N  G  Q

2801 GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
     CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC TGTTCTCGTC CACCGTCGTC
 410   P  E  N   N  Y  K  T   T  P  P   V  L  D   S  D  G  S   F  F  L   Y  S  K   L  T  V  D   K  S  R   W  Q  Q

2901 GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATAAGCA TGCGACGGCC
     CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCCC ATTTATTCGT ACGCTGCCGG
 443 G  N  V  F   S  C  S   V  M  H   E  A  L  H   N  H  Y   T  Q  K   S  L  S  L   S  P  G   K  O

3001 CTAGAGTCCC TAACGCTCGG TTGCCGCCGG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG
     GATCTCAGGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAAACTGT CGAATAGTAG CTATTCGAAA TTACGCCATC AAATAGTGTC

3101 TTAAATTGCT AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG TCACCCTGGA TGCTGTAGGC ATAGGCTTGG
     AATTTAACGA TTGCGTCAGT CCGTGGCACA TACTTTAGAT TGTTACGCGA GTAGCAGTAG GAGCCGTGGC AGTGGGACCT ACGACATCCG TATCCGAACC

3201 TTATGCCGGT ACTGCCGGGC CTCTTGCGGG ATATCGTCCA TT
     AATACGGCCA TGACGGCCCG GAGAACGCCC TATAGCAGGT AA
```

FIG. 2C

```
   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
     AGTGCATTTT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
   1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                              ^STII Signal TIR -1                                          Anti-VEGF Light chain^

 501 CAGTTGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAACTGGT
     GTCAACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCGCGTT CAGTCCTATA ATCGTTGATA AATTTGACCA
  26 Q  L  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  S  A  S  Q  D  I  S  N  Y  L  N  W  Y
                          !

 601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTTCACCTCC TCTCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
     TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
  60   Q  Q  K  P  G  K  A  P  K  V  L  I  Y  F  T  S  S  L  H  S  G  V  P  S  R  F  S  G  S  G  S  G  T

 701 GGATTTCACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGACGTTTGG ACAGGGTACC
     CCTAAAGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGT TGTCATATCG TGGCACGGCA CCTGCAAACC TGTCCCATGG
  93  D  F  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  Y  S  T  V  P  W  T  F  G  Q  G  T

 801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
     TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
 126 K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L

 901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
 160   N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K

1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P  V  T  K  S  F  N  R  G  E  C  O
```

FIG. 3A

```
1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
     GCGTTATACC GCGTTTTACT GGTTGTCGCC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCG GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
     TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT
     ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTTT CCCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
   1                                                                                  M  K  K  N  I  A  F  L  L
                                                                                    ^STII Signal TIR-1

1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
     ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
  10 A  S  M  F  V  F  S  I  A  T  N  A  Y  A  E  V  Q  L  V  E  S  G  G  G  L  V  Q  P  G  G  S  L  R
                                                ^Anti-VEGF Heavy Chain

1701 TTGTCCTGTG CAGCTTCTGG CTACGACTTC ACGCACTACG GTATGAACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA TGGATTAACA
     AACAGGACAC GTCGAAGACC GATGCTGAAG TGCGTGATGC CATACTTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
  43 L  S  C  A  A  S  G  Y  D  F  T  H  Y  G  M  N  W  V  R  Q  A  P  G  K  G  L  E  W  V  G  W  I  N  T

1801 CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTCACT TTTTCTTTAG ACACCTCCAA AAGCACAGCA TACCTGCAGA TGAACAGCCT
     GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAAGTGA AAAAGAAATC TGTGGAGGTT TTCGTGTCGT ATGGACGTCT ACTTGTCGGA
  77   Y  T  G  E  P  T  Y  A  A  D  F  K  R  R  F  T  F  S  L  D  T  S  K  S  T  A  Y  L  Q  M  N  S  L

1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGTACTATT ACGGCACGAG CCACTGGTAT TTCGACGTCT GGGGTCAAGG AACCCTGGTC
     CGCGCGACTC CTGTGACGGC AGATAATGAC ACGTTTCATG GGCATGATAA TGCCGTGCTC GGTGACCATA AAGCTGCAGA CCCCAGTTCC TTGGGACCAG
 110  R  A  E  D  T  A  V  Y  Y  C  A  K  Y  P  Y  Y  Y  G  T  S  H  W  Y  F  D  V  W  G  Q  G  T  L  V

2001 ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA
     TGGCAGAGGA GCCGGAGGTG GTTCCCGGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTC TCGTGGAGAC CCCCGTGTCG CCGGGACCCG ACGGACCAGT
 143 T  V  S  S  A  S  T  K  G  P  S  V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L  G  C  L  V  K

2101 AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCCT CAGGACTCTA
     TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA GGGCCGACAG GATGTCAGGA GTCCTGAGAT
 177   D  Y  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y

2201 CTCCCTCAGC AGCGTGGTGA CTGTGCCCTC TAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG
     GAGGGAGTCG TCGCACCACT GACACGGGAG ATCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGGT CGTTGTGGTT CCACCTGTTC
 210  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T  K  V  D  K

2301 AAAGTTGAGC CCAAATCTTG TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG GACCGTCAGT CTTCCTCTTC CCCCCAAAAC
     TTTCAACTCG GGTTTAGAAC ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG
 243 K  V  E  P  K  S  C  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P

2401 CCAAGGACAC CCTCATGATC TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC AAGTTCAACT GGTACGTGGA
     GGTTCCTGTG GGAGTACTAG AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT GGGACTCCAG TTCAAGTTGA CCATGCACCT
 277   K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D
```

FIG. 3B

```
2501 CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG
     GCCGCACCTC CACGTATTAC GGTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCGTGCAT GGCACACCAG TCGCAGGAGT GGCAGGACGT GGTCCTGACC
 310 G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L  H  Q  D  W

2601 CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAACCAC
     GACTTACCGT TCCTCATGTT CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG
 343 L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q

2701 AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT CCCAGCGACA TCGCCGTGGA
     TCCACATGTG GGACGGGGGT AGGGCCCTTC TCTACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT TCCGAAGATA GGGTCGCTGT AGCGGCACCT
 377  V  Y  T  L  P  P  S  R  E  E  M  T  K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V  E

2801 GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC
     CACCCTCTCG TTACCCGTCG GCCTCTTGTT GATGTTCTGG TGCGGAGGGC ACGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTCGTTCGA GTGGCACCTG
 410 W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D

2901 AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA
     TTCTCGTCCA CCGTCGTCCC CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT
 443 K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K

3001 AATAAGCATG CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA
     TTATTCGTAC GCTGCCGGGA TCTCAGGGAT TGCGAGCCAA CGGCGGCCCG CAAAAAATAA CAATTGAGTA CAAACTGTCG AATAGTAGCT ATTCGAAATT
 477  O

3101 TGCGGTAGTT TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG
     ACGCCATCAA ATAGTGTCAA TTTAACGATT GCGTCAGTCC GTGGCACATA CTTTAGATTG TTACGCGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC
                                                                ^Start Tet Resistance Coding Sequence

3201 CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT
     GACATCCGTA TCCGAACCAA TACGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA GGCTGTCGTA GCGGTCAGTG ATACCGCACG ACGATCGCGA

3301
```

FIG. 3C

```
 1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
   CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
    CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
    CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
    TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
    AGTGCATTTT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
  1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                             ^STII Signal TIR -1                                                        ^Light chain

501 CAGTTGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAACTGGT
    GTCAACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCGCGTT CAGTCCTATA ATCGTTGATA AATTTGACCA
 26 Q  L  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  S  A  S  Q  D  I  S  N  Y  L  N  W  Y

601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTTCACCTCC TCTCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
    TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
 60   Q  Q  K  P  G  K  A  P  K  V  L  I  Y  F  T  S  S  L  H  S  G  V  P  S  R  F  S  G  S  G  S  G  T

701 GGATTTCACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGACGTTTGG ACAGGGTACC
    CCTAAAGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGT TGTCATATCG TGGCACGGCA CCTGCAAACC TGTCCCATGG
 93 D  F  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  Y  S  T  V  P  W  T  F  G  Q  G  T

801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
    TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
126 K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L

901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
    ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
160   N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K

1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
193  D  S  T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S
```

FIG. 4A

```
1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193 D S T  Y S L S  S T L  T L S  K A D Y  E K H  K V Y  A C E V  T H Q  G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P V T  K S F  N R G  E C O

                                                                                                  lambda t0 terminator^

1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
     GCGTTATACC GCGTTTTACT GGTTGTCGCC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCG GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
     TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT
     ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTTT CCCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
   1                                                                                                  M K  K N I A  F L L
                                                                                                      ^STII Signal TIR-1

1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
     ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
  10 A S M  F V F S  I A T  N A Y  A E V Q  L V E  S G G  G L V Q  P G G  S L R
                                                 ^start heavy chain

1701 TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG GTATAAACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA TGGATTAACA
     AACAGGACAC GTCGAAGACC GATATGGAAG TGGTTGATAC CATATTTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
 43 L S C A  A S G  Y T F  T N Y G  I N W  V R Q  A P G K  G L E  W V G  W I N T

1801 CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTCACT TTTTCTTTAG ACACCTCCAA AAGCACAGCA TACCTGCAGA TGAACAGCCT
     GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAAGTGA AAAAGAAATC TGTGGAGGTT TTCGTGTCGT ATGGACGTCT ACTTGTCGGA
 77  Y T G  E P T  Y A A D  F K R  R F T  F S L D  T S K  S T A  Y L Q M  N S L

1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGCACTATT ATGTGAACGA GCGGAAGAGC CACTGGTATT TCGACGTCTG GGGTCAAGGA
     CGCGCGACTC CTGTGACGGC AGATAATGAC ACGTTTCATG GGCGTGATAA TACACTTGCT CGCCTTCTCG GTGACCATAA AGCTGCAGAC CCCAGTTCCT
110 R A E  D T A V  Y Y C  A K Y  P H Y Y  V N E  R K S  H W Y F  D V W  G Q G

2001 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT
     TGGGACCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA
143 T L V T  V S S  A S T  K G P S  V F P  L A P  S S K S  T S G  G T A  A L G C

2101 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC
     CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG
177  L V K  D Y F  P E P V  T V S  W N S  G A L T  S G V  H T F  P A V L  Q S S
```

FIG. 4B

```
2101 GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC
     CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG GGCCGACAGG ATGTCAGGAG
 177   L  V  K   D  Y  F   P  E  P  V   T  V  S   W  N  S   G  A  L  T   S  G  V   H  T  F   P  A  V  L   Q  S  S

2201 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC TGTGCCCTCT AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
     TCCTGAGATG AGGGAGTCGT CGCACCACTG ACACGGGAGA TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC
 210   G  L  Y   S  L  S  S   V  V  T   V  P  S   S  S  L  G   T  Q  T   Y  I  C   N  V  N  H   K  P  S   N  T  K

2301 GTGGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC TTCCTCTTCC
     CACCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTTGAG TGTGTACGGG TGGCACGGGT CGTGGACTTG AGGACCCCCC TGGCAGTCAG AAGGAGAAGG
 243 V  D  K  K   V  E  P   K  S  C   D  K  T  H   T  C  P   P  C  P   A  P  E  L   L  G  G   P  S  V   F  L  F  P

2401 CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG
     GGGGTTTTGG GTTCCTGTGG GAGTACTAGA GGGCCTGGGG ACTCCAGTGT ACGCACCACC ACCTGCACTC GGTGCTTCTG GGACTCCAGT TCAAGTTGAC
 277   P  K  P   K  D  T   L  M  I  S   R  T  P   E  V  T   C  V  V  V   D  V  S   H  E  D   P  E  V  K   F  N  W

2501 GTACGTGGAC GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC
     CATGCACCTG CCGCACCTCC ACGTATTACG GTTCTGTTTC GGCGCCCTCC TCGTCATGTT GTCGTGCATG GCACACCAGT CGCAGGAGTG GCAGGACGTG
 310   Y  V  D   G  V  E  V   H  N  A   K  T  K   P  R  E  E   Q  Y  N   S  T  Y   R  V  V  S   V  L  T   V  L  H

2601 CAGGACTGGC TGAATGGCAA GGAGTACAAG TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA GGGCAGCCCC
     GTCCTGACCG ACTTACCGTT CCTCATGTTC ACGTTCCAGA GGTTGTTTCG GGAGGGTCGG GGGTAGCTCT TTTGGTAGAG GTTTCGGTTT CCCGTCGGGG
 343 Q  D  W  L   N  G  K   E  Y  K   C  K  V  S   N  K  A   L  P  A   P  I  E  K   T  I  S   K  A  K   G  Q  P  R

2701 GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGAAGA GATGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT
     CTCTTGGTGT CCACATGTGG GACGGGGGTA GGGCCCTTCT CTACTGGTTC TTGGTCCAGT CGGACTGGAC GGACCAGTTT CCGAAGATAG GGTCGCTGTA
 377   E  P  Q   V  Y  T   L  P  P  S   R  E  E   M  T  K   N  Q  V  S   L  T  C   L  V  K   G  F  Y  P   S  D  I

2801 CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC
     GCGGCACCTC ACCCTCTCGT TACCCGTCGG CCTCTTGTTG ATGTTCTGGT GCGGAGGGCA CGACCTGAGG CTGCCGAGGA AGAAGGAGAT GTCGTTCGAG
 410   A  V  E   W  E  S  N   G  Q  P   E  N  N   Y  K  T  T   P  P  V   L  D  S   D  G  S  F   F  L  Y   S  K  L

2901 ACCGTGGACA AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT
     TGGCACCTGT TCTCGTCCAC CGTCGTCCCC TTGCAGAAGA GTACGAGGCA CTACGTACTC CGAGACGTGT TGGTGATGTG CGTCTTCTCG GAGAGGGACA
 443 T  V  D  K   S  R  W   Q  Q  G   N  V  F  S   C  S  V   M  H  E   A  L  H  N   H  Y  T   Q  K  S   L  S  L  S

3001 CTCCGGGTAA ATAAGCATGC GACGGCCCTA GAGTCCCTAA CGCTCGGTTG CCGCCGGGCG TTTTTTATTG TTAACTCATG TTTGACAGCT TATCATCGAT
     GAGGCCCATT TATTCGTACG CTGCCGGGAT CTCAGGGATT GCGAGCCAAC GGCGGCCCGC AAAAAATAAC AATTGAGTAC AAACTGTCGA ATAGTAGCTA
 477   P  G  K   O

                                                ^lambda terminator

3101 AAGCTTTAAT GCGGTAGTTT ATCACAGTTA AATTGCTAAC GCAGTCAGGC ACCGTGTATG AAATCTAACA ATGCGCTCAT CGTCATCCTC GGCACCGTCA
     TTCGAAATTA CGCCATCAAA TAGTGTCAAT TTAACGATTG CGTCAGTCCG TGGCACATAC TTTAGATTGT TACGCGAGTA GCAGTAGGAG CCGTGGCAGT

3201 CCCTGGATGC TGTAGGCATA GGCTTGGTTA TGCCGGTACT GCCGGGCCTC TTGCG
     GGGACCTACG ACATCCGTAT CCGAACCAAT ACGGCCATGA CGGCCCGGAG AACGC
```

FIG. 4C

```
3201 CCCTGGATGC TGTAGGCATA GGCTTGGTTA TGCCGGTACT GCCGGGCCTC TTGCG
     GGGACCTACG ACATCCGTAT CCGAACCAAT ACGGCCATGA CGGCCCGGAG AACGC
```

FIG. 4D

```
   1 ATCGATGAAT TCATGCTGTG GTGTCATGGT CGGTGATCGC CAGGGTGCCG ACGCGCATCT CGACTGCACG GTGCACCAAT GCTTCTGGCG TCAGGCAGCC
     TAGCTACTTA AGTACGACAC CACAGTACCA GCCACTAGCG GTCCCACGGC TGCGCGTAGA GCTGACGTGC CACGTGGTTA CGAAGACCGC AGTCCGTCGG
     ^ClaI

 101 ATCGGAAGCT GTGGTATGGC TGTGCAGGTC GTAAATCACT GCATAATTCG TGTCGCTCAA GGCGCACTCC CGTTCTGGAT AATGTTTTTT GCGCCGACAT
     TAGCCTTCGA CACCATACCG ACACGTCCAG CATTTAGTGA CGTATTAAGC ACAGCGAGTT CCGCGTGAGG GCAAGACCTA TTACAAAAAA CGCGGCTGTA

 201 CATAACGGTT CTGGCAAATA TTCTGAAATG AGCTGTTGAC AATTAATCAT CGAACTAGTT TAATGTGTGG AATTGTGAGC GGATAACAAT TAAGCTTAGG
     GTATTGCCAA GACCGTTTAT AAGACTTTAC TCGACAACTG TTAATTAGTA GCTTGATCAA ATTACACACC TTAACACTCG CCTATTGTTA ATTCGAATCC

 301 ATTCTAGAGG GAAGATTTAT GAAATCACTG TTTAAAGTAA CGCTGCTGGC GACCACAATG GCCGTTGCCC TGCATGCACC AATCACTTTT GCTGCTGAAG
     TAAGATCTCC CTTCTAAATA CTTTAGTGAC AAATTTCATT GCGACGACCG CTGGTGTTAC CGGCAACGGG ACGTACGTGG TTAGTGAAAA CGACGACTTC
   1                   M  K  S  L  F  K  V  T  L  L  A  T  T  M  A  V  A  L  H  A  P  I  T  F  A  A  E  A
                       ^fkpA start

 401 CTGCAAAACC TGCTACAGCT GCTGACAGCA AAGCAGCGTT CAAAAATGAC GATCAGAAAT CAGCTTATGC ACTGGGTGCC TCGCTGGGTC GTTACATGGA
     GACGTTTTGG ACGATGTCGA CGACTGTCGT TTCGTCGCAA GTTTTTACTG CTAGTCTTTA GTCGAATACG TGACCCACGG AGCGACCCAG CAATGTACCT
  29   A  K  P  A  T  A  A  D  S  K  A  A  F  K  N  D  D  Q  K  S  A  Y  A  L  G  A  S  L  G  R  Y  M  E

 501 AAACTCTCTA AAAGAACAAG AAAAACTGGG CATCAAACTG GATAAAGATC AGCTGATCGC TGGTGTTCAG GATGCATTTG CTGATAAGAG CAAACTCTCC
     TTTGAGAGAT TTTCTTGTTC TTTTTGACCC GTAGTTTGAC CTATTTCTAG TCGACTAGCG ACCACAAGTC CTACGTAAAC GACTATTCTC GTTTGAGAGG
  62 N  S  L  K  E  Q  E  K  L  G  I  K  L  D  K  D  Q  L  I  A  G  V  Q  D  A  F  A  D  K  S  K  L  S

 601 GACCAAGAGA TCGAACAGAC TCTACAAGCA TTCGAAGCTC GCGTGAAGTC TTCTGCTCAG GCGAAGATGG AAAAAGACGC GGCTGATAAC GAAGCAAAAG
     CTGGTTCTCT AGCTTGTCTG AGATGTTCGT AAGCTTCGAG CGCACTTCAG AAGACGAGTC CGCTTCTACC TTTTTCTGCG CCGACTATTG CTTCGTTTTC
  95 D  Q  E  I  E  Q  T  L  Q  A  F  E  A  R  V  K  S  S  A  Q  A  K  M  E  K  D  A  A  D  N  E  A  K  G

 701 GTAAAGAGTA CCGCGAGAAA TTTGCCAAAG AGAAAGGTGT GAAAACCTCT TCAACTGGTC TGGTTTATCA GGTAGTAGAA GCCGGTAAAG GCGAAGCACC
     CATTTCTCAT GGCGCTCTTT AAACGGTTTC TCTTTCCACA CTTTTGGAGA AGTTGACCAG ACCAAATAGT CCATCATCTT CGGCCATTTC CGCTTCGTGG
 129   K  E  Y  R  E  K  F  A  K  E  K  G  V  K  T  S  S  T  G  L  V  Y  Q  V  V  E  A  G  K  G  E  A  P

 801 GAAAGACAGC GATACTGTTG TAGTGAACTA CAAAGGTACG CTGATCGACG GTAAAGAGTT CGACAACTCT TACACCCGTG GTGAACCGCT TTCTTTCCGT
     CTTTCTGTCG CTATGACAAC ATCACTTGAT GTTTCCATGC GACTAGCTGC CATTTCTCAA GCTGTTGAGA ATGTGGGCAC CACTTGGCGA AAGAAAGGCA
 162   K  D  S  D  T  V  V  V  N  Y  K  G  T  L  I  D  G  K  E  F  D  N  S  Y  T  R  G  E  P  L  S  F  R

 901 CTGGACGGTG TTATCCCGGG TTGGACAGAA GGTCTGAAGA ACATCAAGAA AGGCGGTAAG ATCAAACTGG TTATTCCACC AGAACTGGCT TACGGCAAAG
     GACCTGCCAC AATAGGGCCC AACCTGTCTT CCAGACTTCT TGTAGTTCTT TCCGCCATTC TAGTTTGACC AATAAGGTGG TCTTGACCGA ATGCCGTTTC
 195 L  D  G  V  I  P  G  W  T  E  G  L  K  N  I  K  K  G  G  K  I  K  L  V  I  P  P  E  L  A  Y  G  K  A
```

FIG. 5A

```
1001 CGGGTGTTCC GGGGATCCCA CCGAATTCTA CCCTGGTGTT TGACGTAGAG CTGCTGGATG TGAAACCAGC GCCGAAGGCT GATGCAAAGC CGGAAGCTGA
     GCCCACAAGG CCCCTAGGGT GGCTTAAGAT GGGACCACAA ACTGCATCTC GACGACCTAC ACTTTGGTCG CGGCTTCCGA CTACGTTTCG GCCTTCGACT
 229   G  V  P   G  I  P   P  N  S  T   L  V  F   D  V  E   L  L  D  V   K  P  A   P  K  A   D  A  K  P   E  A  D

1101 TGCGAAAGCC GCAGATTCTG CTAAAAAATA AAAGCTAGC
     ACGCTTTCGG CGTCTAAGAC GATTTTTTAT TTTCGATCG
 262  A  K  A   A  D  S  A   K  K  O
                                    ^NheI
```

FIG. 5B

```
   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA
     ^EcoRI

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATCTA GAATTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
     AGTGCATTTT TCCCATAGAT CTTAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
   1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                              ^start STII signal TIR 7                                    anti-TF light chain^

 501 CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACTGGT
     GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA
  26 Q  M  T  Q   S  P  S   S  L  S   A  S  V  G   D  R  V   T  I  T   C  R  A  S   R  D  I   K  S  Y   L  N  W  Y

 601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
     TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
  60   Q  Q  K   P  G  K   A  P  K  V   L  I  Y   Y  A  T   S  L  A  E   G  V  P   S  R  F   S  G  S  G   S  G  T

 701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
     CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCCT CTCAGAGGTA CCTGTAAACC TGTCCCATGG
  93   D  Y  T   L  T  I   S  S  L  Q   P  E  D   F  A  T   Y  Y  C  L   Q  H  G   E  S  P  W   T  F  G   Q  G  T

 801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
     TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
 126 K  V  E  I   K  R  T   V  A  A   P  S  V  F   I  F  P   P  S  D   E  Q  L  K   S  G  T   A  S  V   V  C  L  L

 901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
 160   N  N  F   Y  P  R   E  A  K  V   Q  W  K   V  D  N   A  L  Q  S   G  N  S   Q  E  S   V  T  E  Q   D  S  K
```

FIG. 6A

```
1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T   Y  S  L  S   S  T  L   T  L  S   K  A  D  Y   E  K  H   K  V  Y   A  C  E  V   T  H  Q   G  L  S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P  V  T   K  S  F   N  R  G   E  C  O
                                                                                    lambda t0 terminator^

1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGACTG CACGGTGCAC CAATGCTTCT GGCGTCAGGC AGCCATCGGA AGCTGTGGTA
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGGTAGCCT TCGACACCAT

1301 TGGCTGTGCA GGTCGTAAAT CACTGCATAA TTCGTGTCGC TCAAGGCGCA CTCCCGTTCT GGATAATGTT TTTTGCGCCG ACATCATAAC GGTTCTGGCA
     ACCGACACGT CCAGCATTTA GTGACGTATT AAGCACAGCG AGTTCCGCGT GAGGGCAAGA CCTATTACAA AAAACGCGGC TGTAGTATTG CCAAGACCGT

1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAACT AGTTTAATGT GTGGAATTGT GAGCGGATAA CAATTAAGCT TAGGATCTAG AATTATGAAG
     TTATAAGACT TTACTCGACA ACTGTTAATT AGTAGCTTGA TCAAATTACA CACCTTAACA CTCGCCTATT GTTAATTCGA ATCCTAGATC TTAATACTTC
   1                                                                                                    M  K
                                                                                        Start STII signal TIR 3^

1501 AAGAATATTG CGTTCCTACT TGCCTCTATG TTTGTCTTTT CTATAGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC
     TTCTTATAAC GCAAGGATGA ACGGAGATAC AAACAGAAAA GATATCGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG
   3 K  N  I  A   F  L  L   A  S  M   F  V  F  S   I  A  T   N  A  Y   A  E  V  Q   L  V  E   S  G  G   G  L  V  Q
                                                                                    ^anti-TF heavy chain

1601 AGCCAGGGGG CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA
     TCGGTCCCCC GAGTGAGGCA AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT
  37   P  G  G   S  L  R   L  S  C  A   A  S  G   F  N  I   K  E  Y  Y   M  H  W   V  R  Q   A  P  G  K   G  L  E

1701 ATGGGTTGGA TTGATTGATC CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA
     TACCCAACCT AACTAACTAG GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGCGAC TGTTAAGGTT TTTGTGTCGT
  70  W  V  G   L  I  D  P   E  Q  G   N  T  I   Y  D  P  K   F  Q  D   R  A  T   I  S  A  D   N  S  K   N  T  A

1801 TACCTGCAGA TGAACAGCCT GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCTGG
     ATGGACGTCT ACTTGTCGGA CGCACGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCCAGTT CCTTGGGACC
 103 Y  L  Q  M   N  S  L   R  A  E   D  T  A  V   Y  Y  C   A  R  D   T  A  A  Y   F  D  Y   W  G  Q   G  T  L  V

1901 TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT
     AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA
 137  T  V  S   S  A  S   T  K  G  P   S  V  F   P  L  A   P  S  S  K   S  T  S   G  G  T   A  A  L  G   C  L  V
                              ^ApaI

2001 CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
     GTTCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG
 170  K  D  Y   F  P  E  P   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S   S  G  L
```

FIG. 6B

```
2101 TACTCCCTCA GCAGCGTGGT GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA
     ATGAGGGAGT CGTCGCACCA CTGACACGGG AGATCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT
 203 Y  S  L  S   S  V  V   T  V  P   S  S  S  L   G  T  Q   T  Y  I   C  N  V  N   H  K  P   S  N  T   K  V  D  K

2201 AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA
     TCTTTCAACT CGGGTTTAGA ACACTGTTTT GAGTGTGTAC GGGTGGCACG GGTCGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGGTTT
 237   K  V  E   P  K  S   C  D  K  T   H  T  C   P  P  C   P  A  P  E   L  L  G   G  P  S   V  F  L  F   P  P  K

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
     TGGGTTCCTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC
 270  P  K  D   T  L  M  I   S  R  T   P  E  V   T  C  V  V   V  D  V   S  H  E   D  P  E  V   K  F  N   W  Y  V

2401 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
     CTGCCGCACC TCCACGTATT ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCCTGA
 303 D  G  V  E   V  H  N   A  K  T   K  P  R  E   E  Q  Y   N  S  T   Y  R  V  V   S  V  L   T  V  L   H  Q  D  W

2501 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC
     CCGACTTACC GTTCCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CGGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG
 337   L  N  G   K  E  Y   K  C  K  V   S  N  K   A  L  P   A  P  I  E   K  T  I   S  K  A   K  G  Q  P   R  E  P

2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG
     TGTCCACATG TGGGACGGGG GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGGTCGCT GTAGCGGCAC
 370  Q  V  Y   T  L  P  P   S  R  E   E  M  T   K  N  Q  V   S  L  T   C  L  V   K  G  F  Y   P  S  D   I  A  V

2701 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG
     CTCACCCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC
 403 E  W  E  S   N  G  Q   P  E  N   N  Y  K  T   T  P  P   V  L  D   S  D  G  S   F  F  L   Y  S  K   L  T  V  D

2801 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG
     TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCCC
 437   K  S  R   W  Q  Q   G  N  V  F   S  C  S   V  M  H   E  A  L  H   N  H  Y   T  Q  K   S  L  S  L   S  P  G

2901 TAAATAAGCA TGCGACGGCC CTAGAGTCCC TAACGCTCGG TTGCCGCCGG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
     ATTTATTCGT ACGCTGCCGG GATCTCAGGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAAACTGT CGAATAGTAG CTATTCGAAA
 470  K  O

3001
```

FIG. 6C

```
   1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
     CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTTCTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
     CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
     CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT
     TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATCTA GAATTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
     AGTGCATTTT TCCCATAGAT CTTAATACTT TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG
   1                          M  K  K  N  I  A  F  L  L  A  S  M  F  V  F  S  I  A  T  N  A  Y  A  D  I
                              ^Start STII signal TIR 7                                    anti-tissue factor light chain^

 501 CAGATGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACTGGT
     GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA
  26 Q  M  T  Q  S  P  S  S  L  S  A  S  V  G  D  R  V  T  I  T  C  R  A  S  R  D  I  K  S  Y  L  N  W  Y

 601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
     TAGTTGTCTT TGGTCCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG
  60   Q  Q  K  P  G  K  A  P  K  V  L  I  Y  Y  A  T  S  L  A  E  G  V  P  S  R  F  S  G  S  G  S  G  T

 701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
     CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCCT CTCAGAGGTA CCTGTAAACC TGTCCCATGG
  93  D  Y  T  L  T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  L  Q  H  G  E  S  P  W  T  F  G  Q  G  T

 801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
     TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
 126 K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V  C  L  L

 901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
     ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT
 160   N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A  L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K

1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
     CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCCGGACTCG
 193  D  S  T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A  C  E  V  T  H  Q  G  L  S
```

FIG. 7A

```
1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCCTCT ACGCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
     AGCGGGCAGT GTTTCTCGAA GTTGTCCCCT CTCACAATTA ATTTAGGAGA TGCGGCCTGC GTAGCACCGC TCGAGCCATG GGCCCCTAGA TCCGGATTGC
 226 S  P  V  T   K  S  F   N  R  G   E  C  O
                                                                                    lambda t0 terminator^

1201 CTCGGTTGCC GCCGGGCGTT TTTTATTGTT GCCGACGCGC ATCTCGACTG CACGGTGCAC CAATGCTTCT GGCGTCAGGC AGCCATCGGA AGCTGTGGTA
     GAGCCAACGG CGGCCCGCAA AAAATAACAA CGGCTGCGCG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGGTAGCCT TCGACACCAT

1301 TGGCTGTGCA GGTCGTAAAT CACTGCATAA TTCGTGTCGC TCAAGGCGCA CTCCCGTTCT GGATAATGTT TTTTGCGCCG ACATCATAAC GGTTCTGGCA
     ACCGACACGT CCAGCATTTA GTGACGTATT AAGCACAGCG AGTTCCGCGT GAGGGCAAGA CCTATTACAA AAAACGCGGC TGTAGTATTG CCAAGACCGT

1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAACT AGTTTAATGT GTGGAATTGT GAGCGGATAA CAATTAAGCT TAGGATCTAG AATTATGAAG
     TTATAAGACT TTACTCGACA ACTGTTAATT AGTAGCTTGA TCAAATTACA CACCTTAACA CTCGCCTATT GTTAATTCGA ATCCTAGATC TTAATACTTC
   1                                                                                                      M  K'
                                                                                          Start STII signal TIR 3^

1501 AAGAATATTG CGTTCCTACT TGCCTCTATG TTTGTCTTTT CTATAGCTAC AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC
     TTCTTATAAC GCAAGGATGA ACGGAGATAC AAACAGAAAA GATATCGATG TTTGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG
   3 K  N  I  A   F  L  L   A  S  M   F  V  F  S   I  A  T   N  A  Y   A  E  V  Q   L  V  E   S  G  G   G  L  V  Q
                    anti-tissue factor heavy chain with cys to ser in hinge^

1601 AGCCAGGGGG CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GGTCCGTCAG GCCCCGGGTA AGGGCCTGGA
     TCGGTCCCCC GAGTGAGGCA AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT
  37   P  G  G   S  L  R   L  S  C  A   A  S  G   F  N  I   K  E  Y  Y   M  H  W   V  R  Q   A  P  G  K   G  L  E

1701 ATGGGTTGGA TTGATTGATC CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA
     TACCCAACCT AACTAACTAG GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGCGAC TGTTAAGGTT TTTGTGTCGT
  70  W  V  G   L  I  D  P   E  Q  G   N  T  I   Y  D  P  K   F  Q  D   R  A  T   I  S  A  D   N  S  K   N  T  A

1801 TACCTGCAGA TGAACAGCCT GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCTGG
     ATGGACGTCT ACTTGTCGGA CGCACGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCCAGTT CCTTGGGACC
 103 Y  L  Q  M   N  S  L   R  A  E   D  T  A  V   Y  Y  C   A  R  D   T  A  A  Y   F  D  Y   W  G  Q   G  T  L  V

1901 TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT
     AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA
 137   T  V  S   S  A  S   T  K  G  P   S  V  F   P  L  A   P  S  S  K   S  T  S   G  G  T   A  A  L  G   C  L  V

2001 CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
     GTTCCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTCAG GAGTCCTGAG
 170  K  D  Y   F  P  E  P   V  T  V   S  W  N   S  G  A  L   T  S  G   V  H  T   F  P  A  V   L  Q  S   S  G  L

2101 TACTCCCTCA GCAGCGTGGT GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA
     ATGAGGGAGT CGTCGCACCA CTGACACGGG AGATCGTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG TTCCACCTGT
 203 Y  S  L  S   S  V  V   T  V  P   S  S  S  L   G  T  Q   T  Y  I   C  N  V  N   H  K  P   S  N  T   K  V  D  K
```

FIG. 7B

```
2201 AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACTAG TCCACCGTCT CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA
     TCTTTCAACT CGGGTTTAGA ACACTGTTTT GAGTGTGATC AGGTGGCAGA GGTCGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGGTTT
 237   K  V  E   P  K  S   C  D  K  T   H  T  S   P  P  S   P  A  P  E   L  L  G   G  P  S   V  F  L  F   P  P  K
                                        ^Hinge cys to ser
                                                    ^Hinge cys to ser

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
     TGGGTTCCTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC
 270  P  K  D   T  L  M  I   S  R  T   P  E  V   T  C  V  V   V  D  V   S  H  E   D  P  E  V   K  F  N   W  Y  V

2401 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
     CTGCCGCACC TCCACGTATT ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCCTGA
 303 D  G  V  E   V  H  N   A  K  T   K  P  R  E   E  Q  Y   N  S  T   Y  R  V  V   S  V  L   T  V  L   H  Q  D  W

2501 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC
     CCGACTTACC GTTCCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CGGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG
 337   L  N  G   K  E  Y   K  C  K  V   S  N  K   A  L  P   A  P  I  E   K  T  I   S  K  A   K  G  Q  P   R  E  P

2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATCGCCGTG
     TGTCCACATG TGGGACGGGG GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGGACTG GACGGACCAG TTTCCGAAGA TAGGGTCGCT GTAGCGGCAC
 370  Q  V  Y   T  L  P  P   S  R  E   E  M  T   K  N  Q  V   S  L  T   C  L  V   K  G  F  Y   P  S  D   I  A  V

2701 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG
    ^CTCACCCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTC GAGTGGCACC
 403 E  W  E  S   N  G  Q   P  E  N   N  Y  K  T   T  P  P   V  L  D   S  D  G  S   F  F  L   Y  S  K   L  T  V  D

2801 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG
     TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTTGGTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCCC
 437   K  S  R   W  Q  Q   G  N  V  F   S  C  S   V  M  H   E  A  L  H   N  H  Y   T  Q  K   S  L  S  L   S  P  G

2901 TAAATAAGCA TGCGACGGCC CTAGAGTCCC TAACGCTCGG TTGCCGCCGG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
     ATTTATTCGT ACGCTGCCGG GATCTCAGGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAAACTGT CGAATAGTAG CTATTCGAAA
 470  K  O

3001
```

FIG. 7C

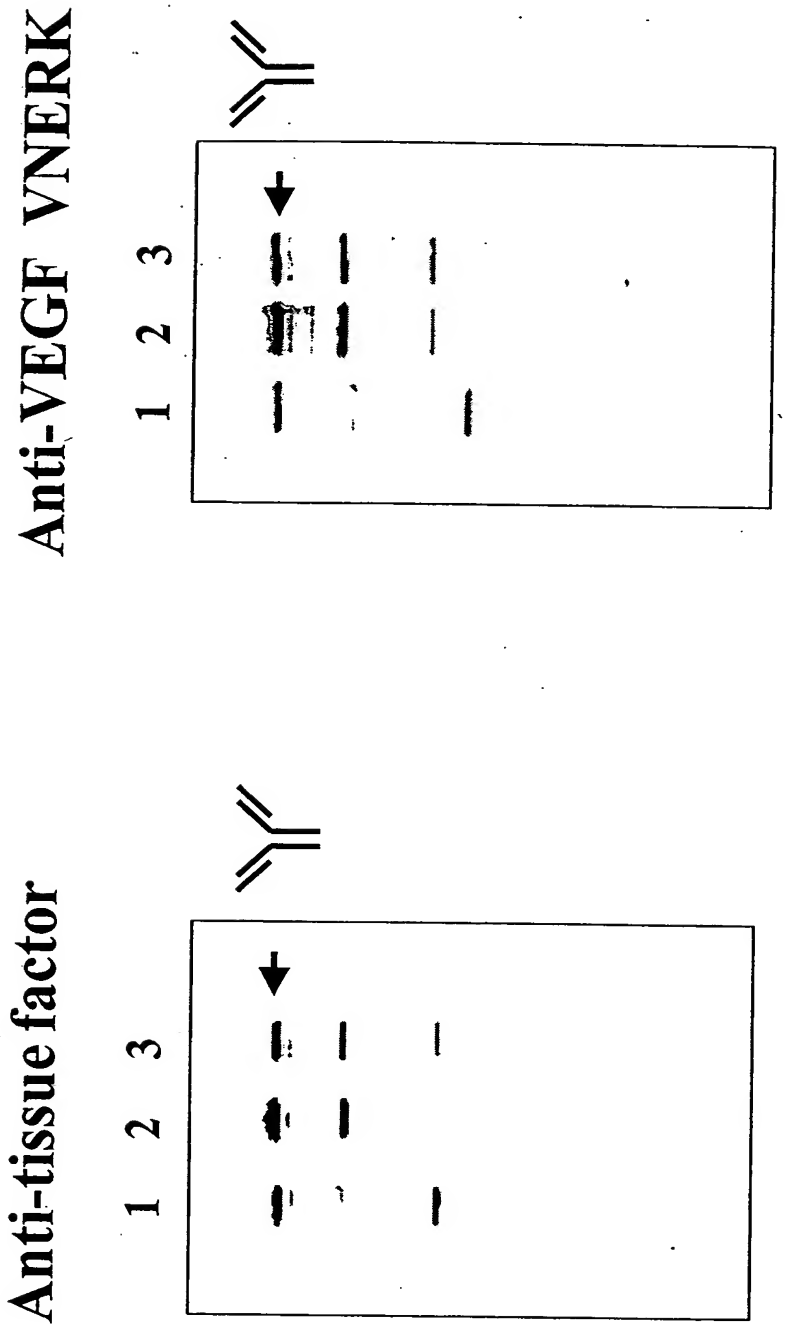

FIG. 8

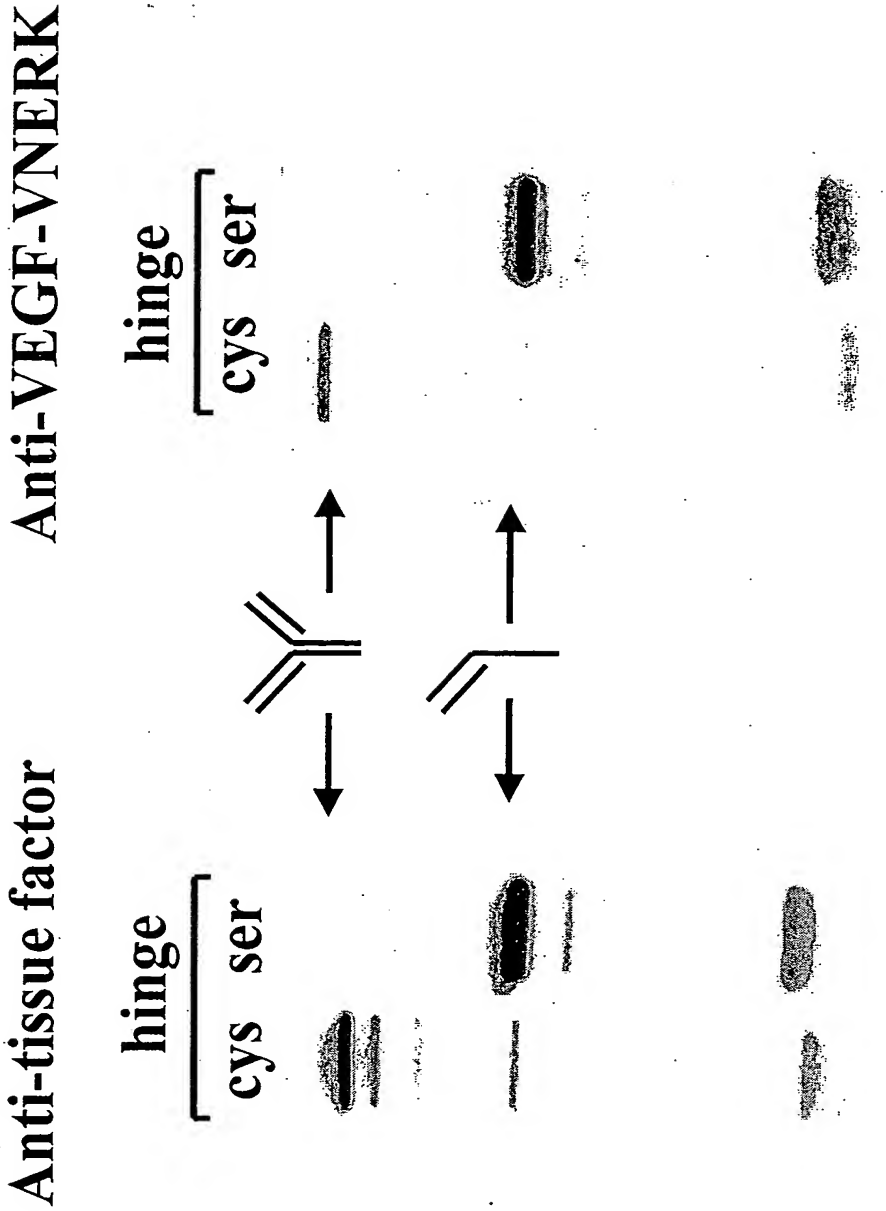
Anti-VEGF-VNERK
hinge
cys ser
Anti-tissue factor
hinge
cys ser

FIG. 9

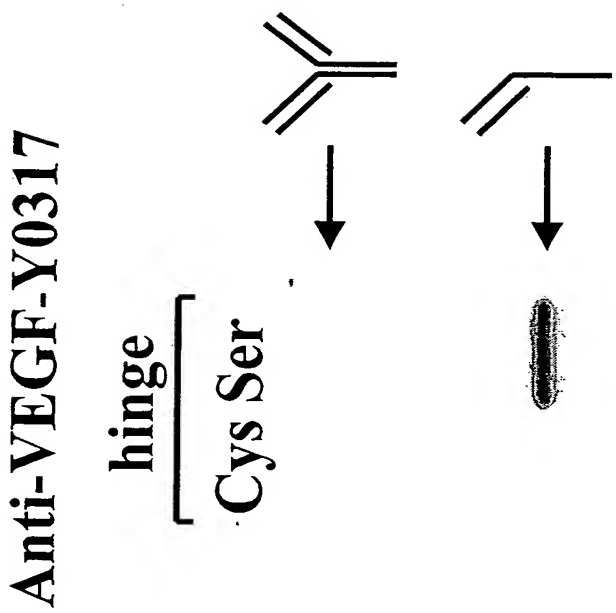

FIG. 10

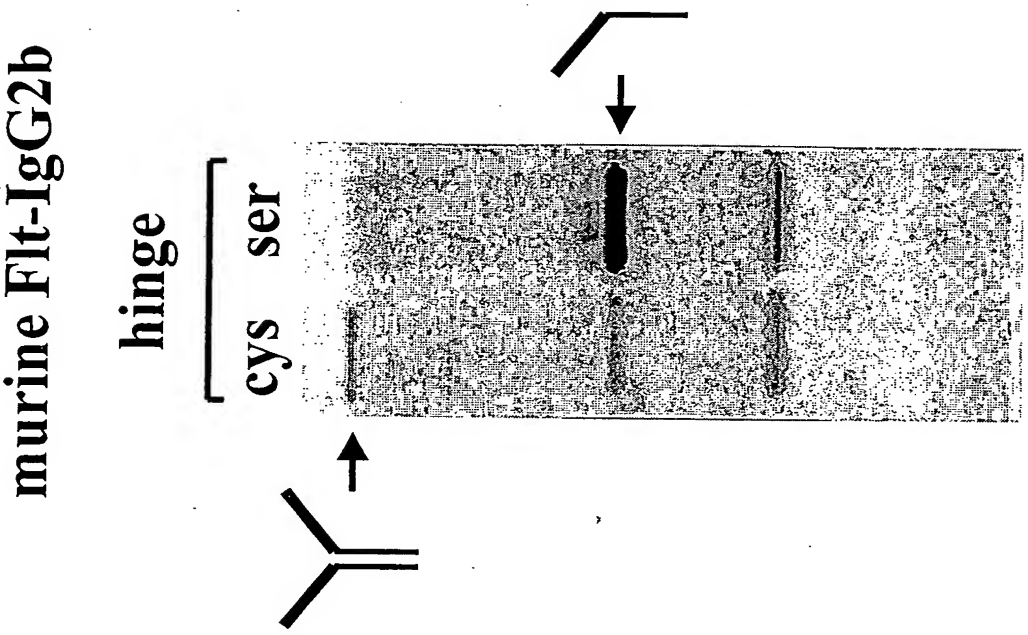

FIG. 11

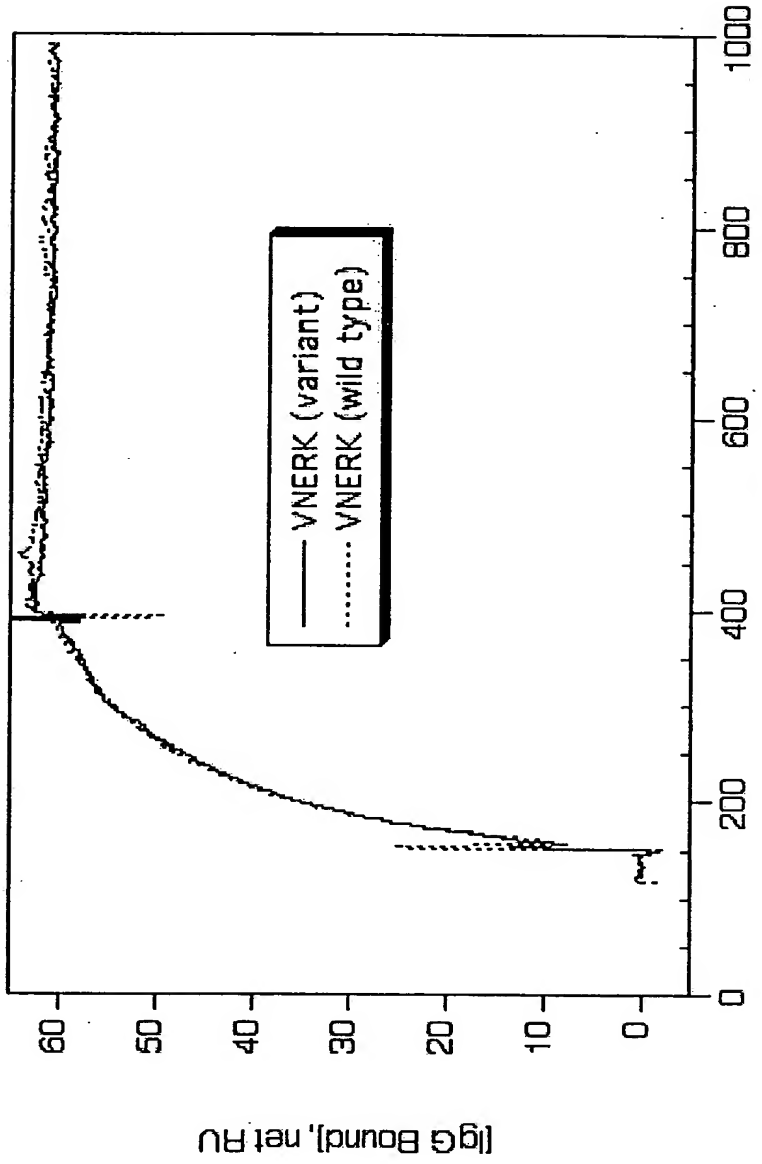
VNERK (variant)
VNERK (wild type)
[IgG Bound], net RU
Time (s)
0
10
20
30
40
50
60
0
200
400
600
800
1000

FIG. 12

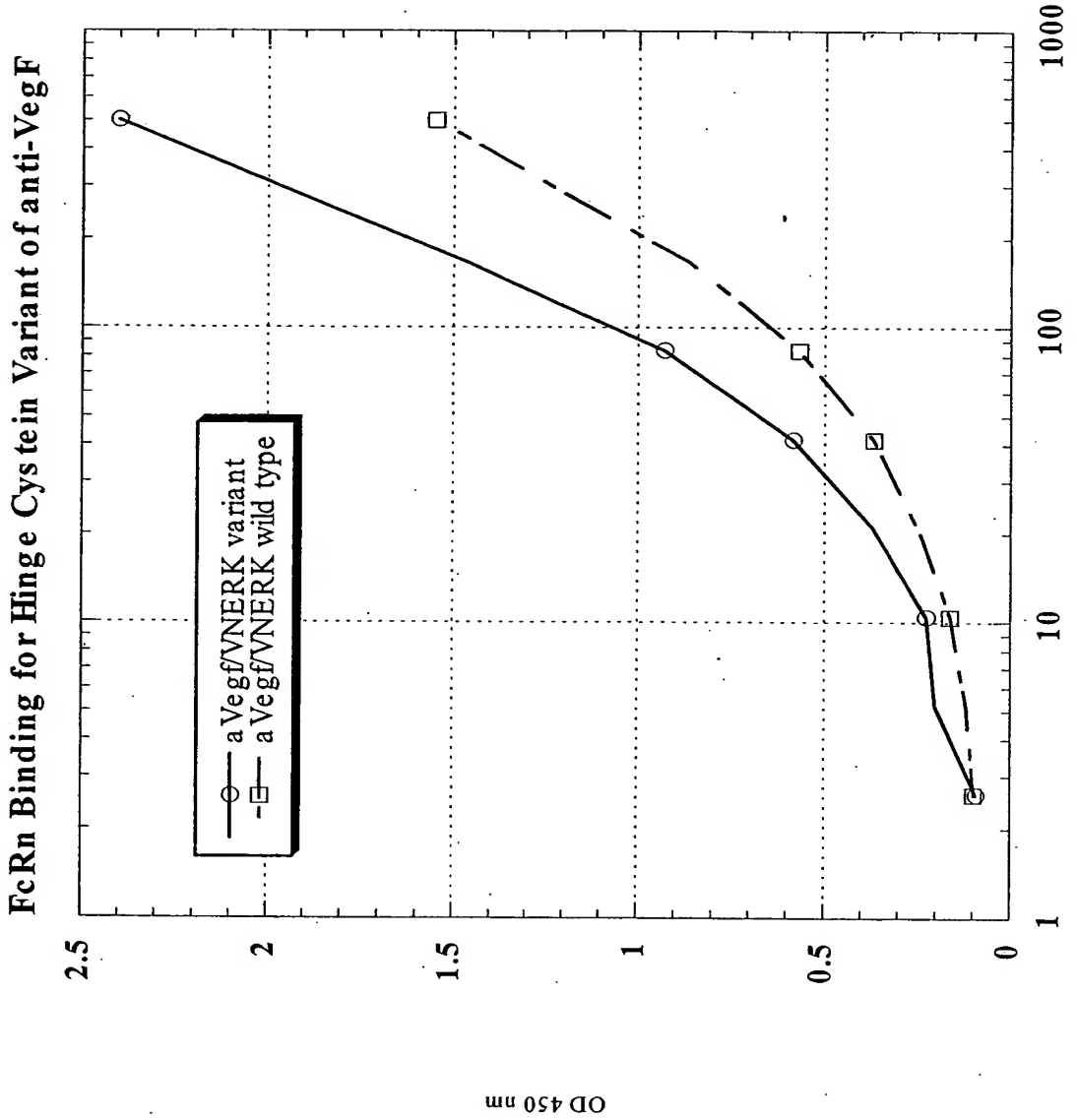
FcRn Binding for Hinge Cysteine Variant of anti-VegF
aVegf/VNERK variant
aVegf/VNERK wild type
OD 450 nm
anti-VegF, ng/ml
2.5
2
1.5
1
0.5
0
1
10
100
1000

FIG. 13

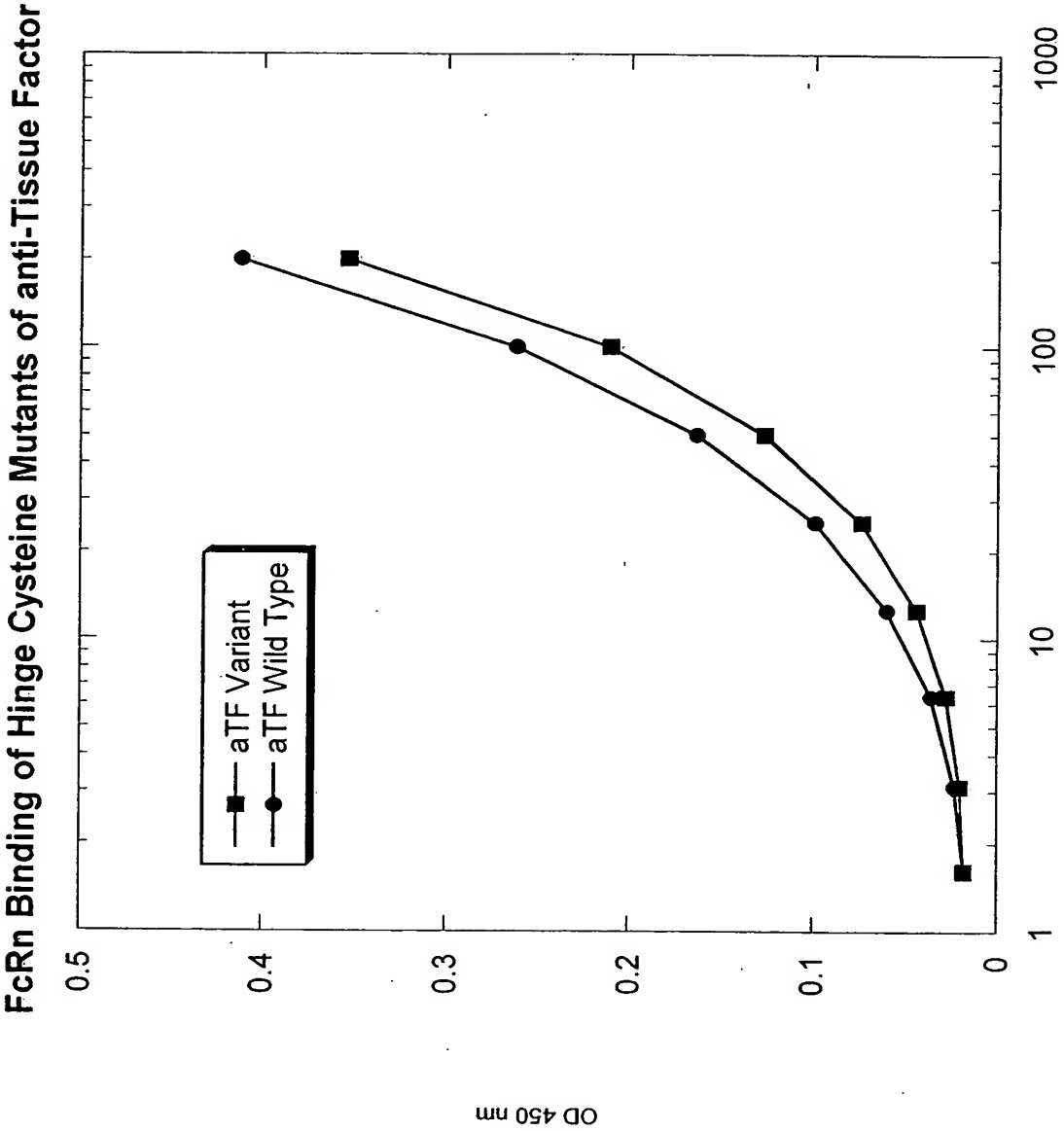
FcRn Binding of Hinge Cysteine Mutants of anti-Tissue Factor
aTF Variant
aTF Wild Type
OD 450 nm
0.5
0.4
0.3
0.2
0.1
0
1
10
100
1000
ATF (ng/ml)

FIG. 14

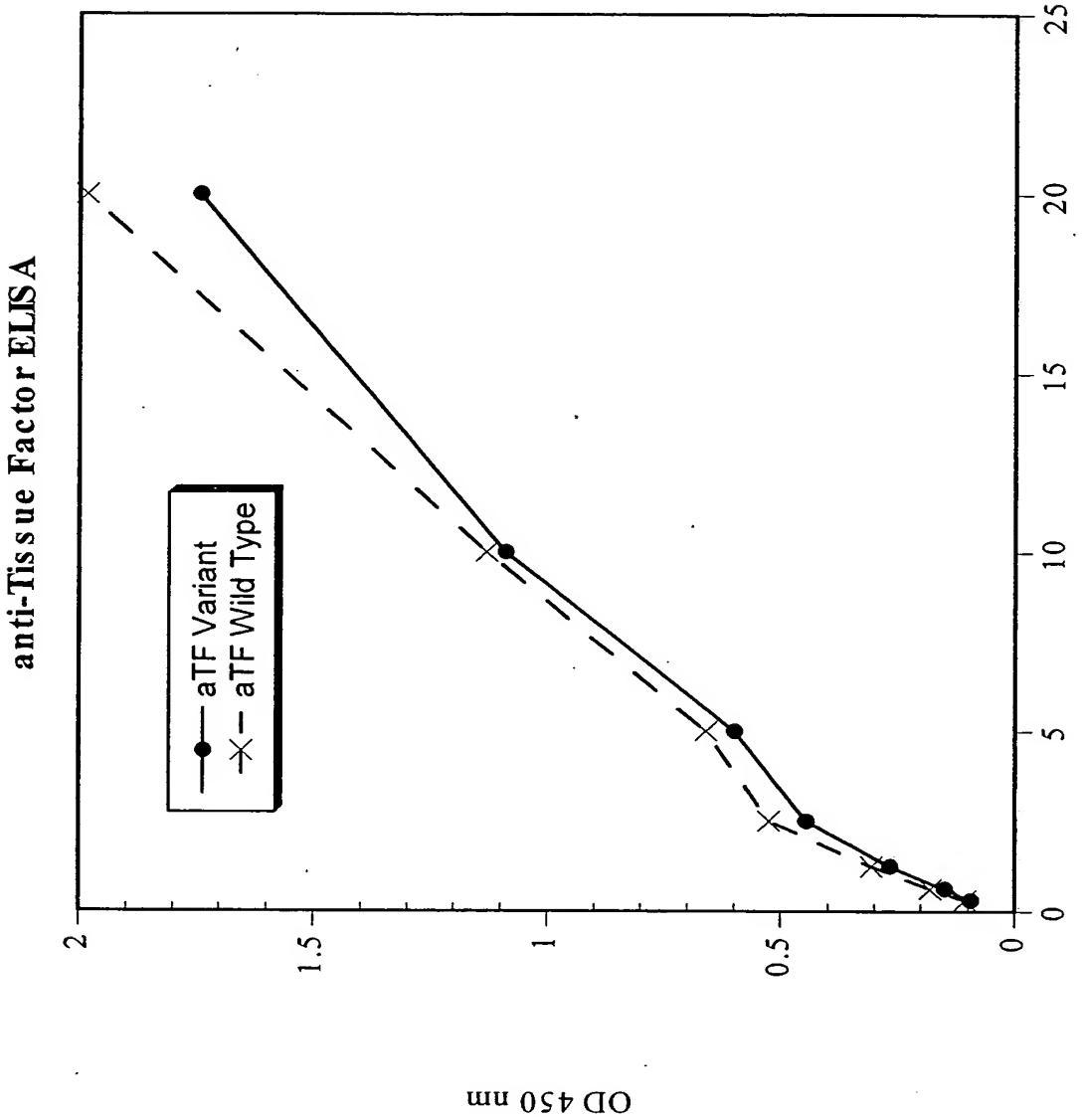
anti-Tissue Factor ELISA
aTF Variant
aTF Wild Type
OD 450 nm
ng/ml
0
0.5
1
1.5
2
0
5
10
15
20
25

FIG. 15

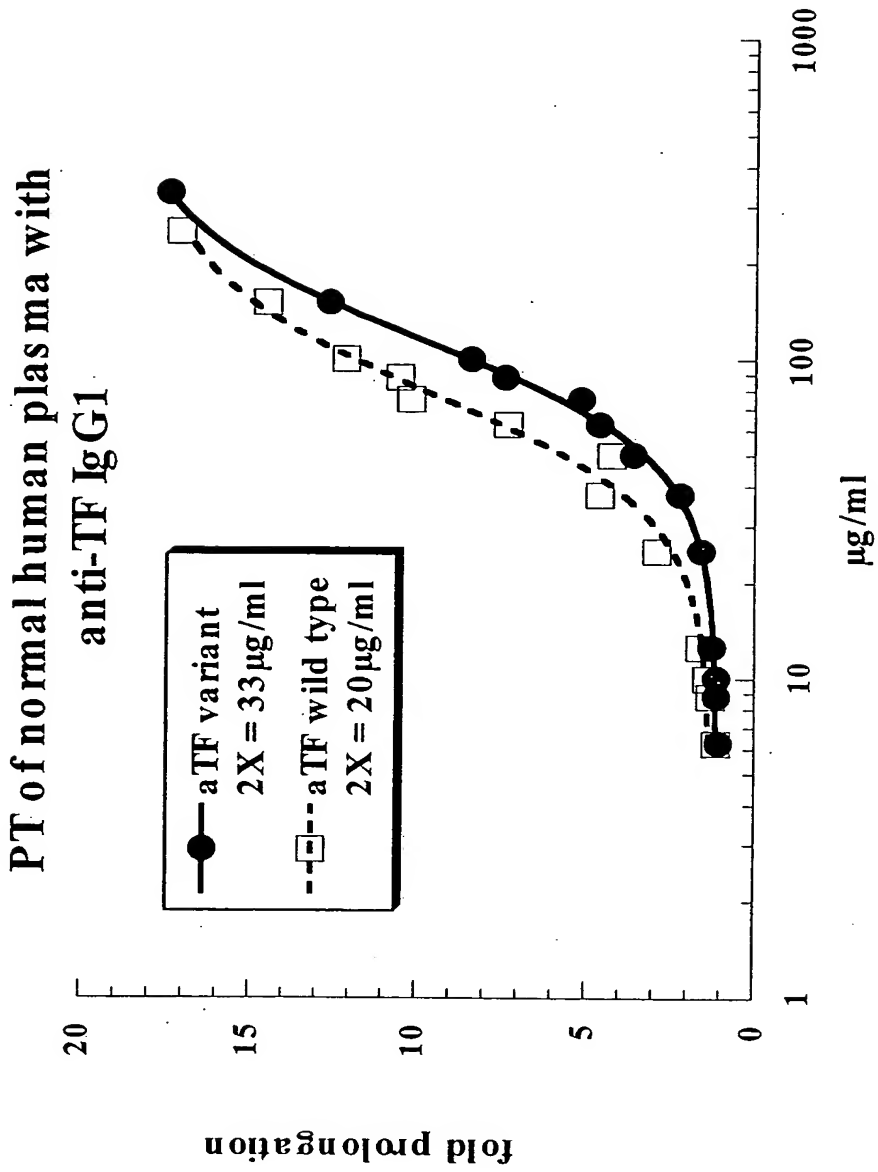
PT of normal human plasma with
anti-TF IgG1
aTF variant
2X = 33 µg/ml
aTF wild type
2X = 20 µg/ml
fold prolongation
0
5
10
15
20
1
10
100
1000
µg/ml

FIG. 16

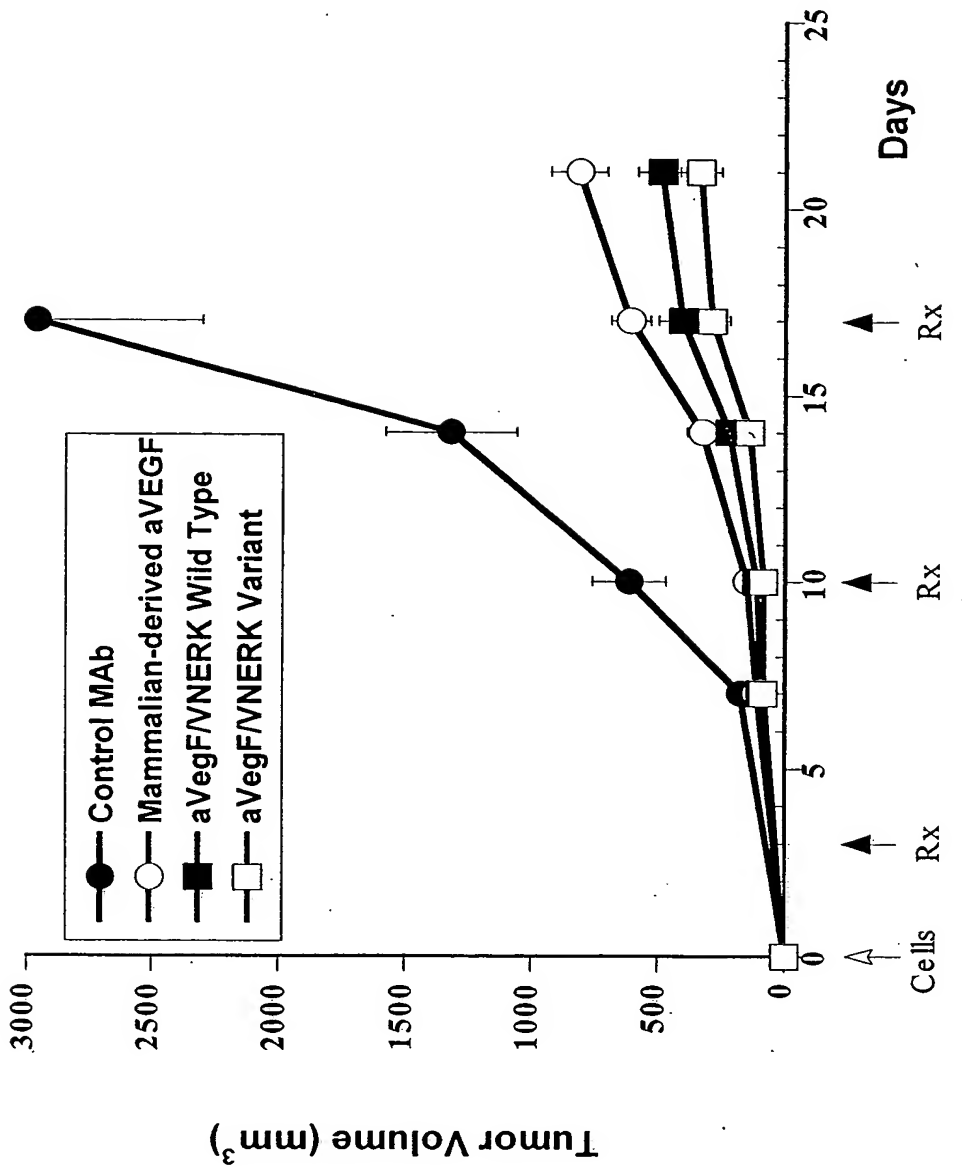
Tumor Volume (mm³)
3000
2500
2000
1500
1000
500
0
Control MAb
Mammalian-derived aVEGF
aVegF/VNERK Wild Type
aVegF/VNERK Variant
Cells
Rx
Rx
Rx
0
5
10
15
20
25
Days

FIG. 17

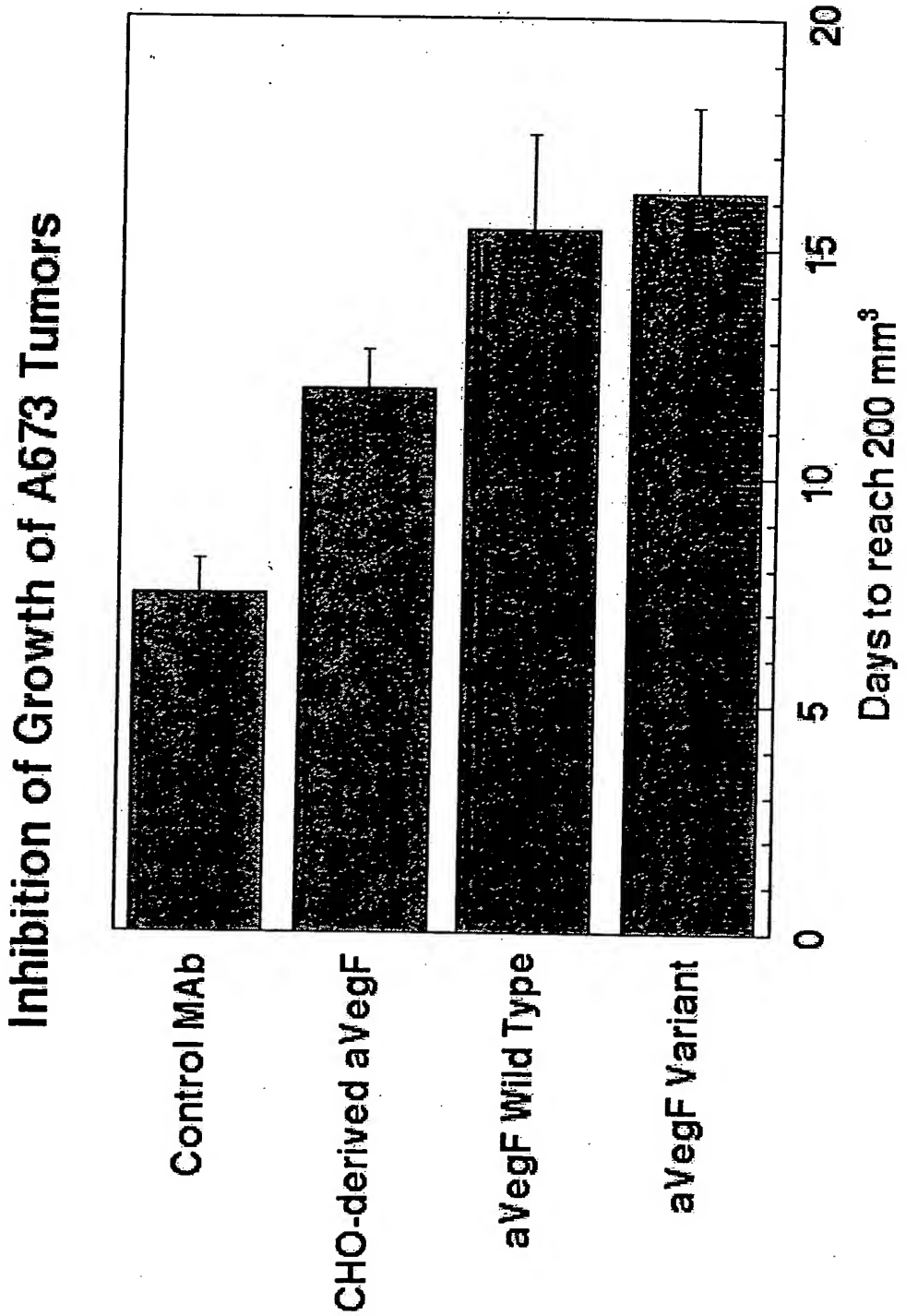
Inhibition of Growth of A673 Tumors
Days to reach 200 mm3
0
5
10
15
20
Control MAb
CHO-derived aVegF
aVegF Wild Type
aVegF Variant

FIG. 18

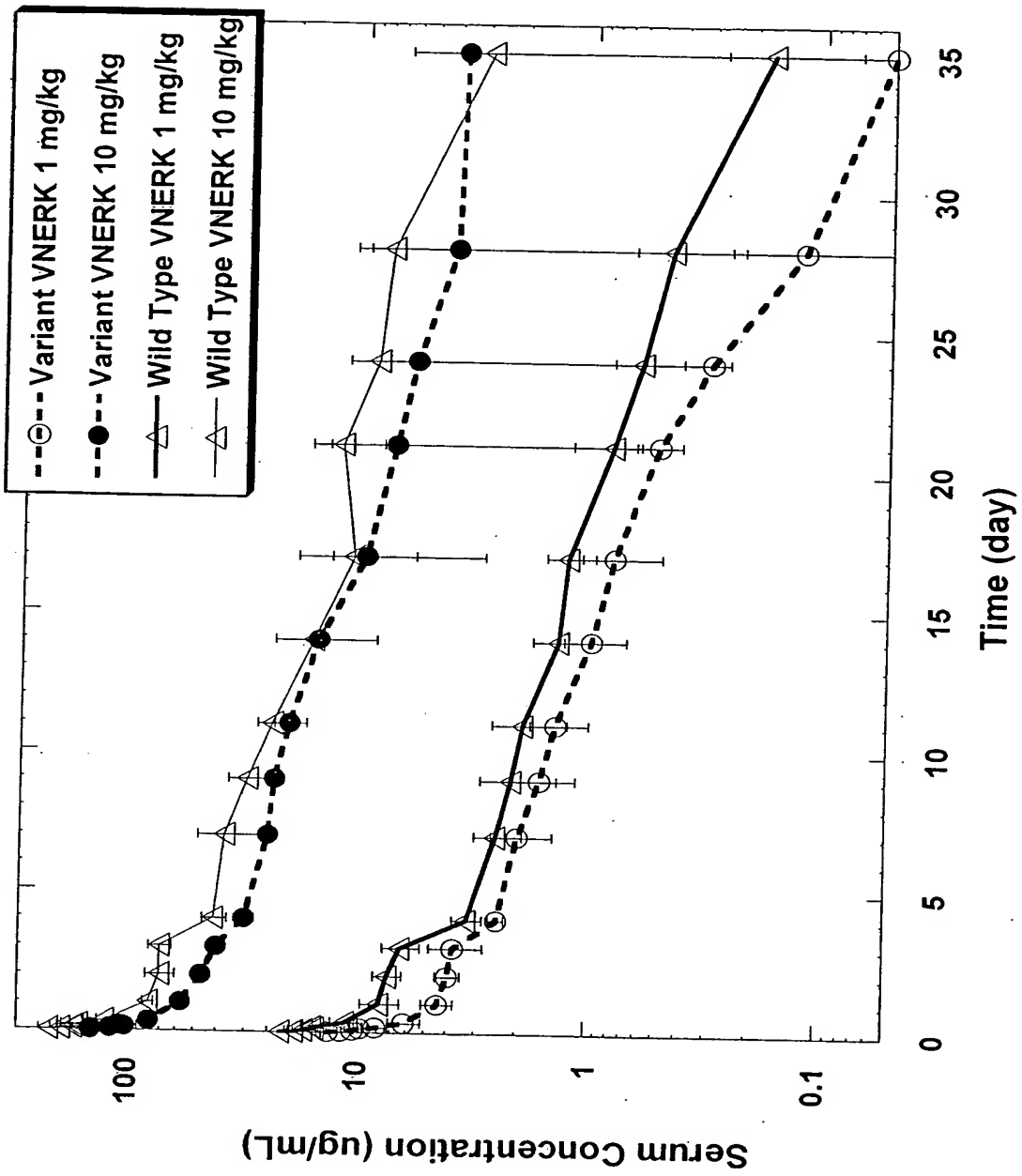
Variant VNERK 1 mg/kg
Variant VNERK 10 mg/kg
Wild Type VNERK 1 mg/kg
Wild Type VNERK 10 mg/kg
Serum Concentration (ug/mL)
100
10
1
0.1
0
5
10
15
20
25
30
35
Time (day)

FIG. 19